10/763,042

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		DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ	
☐	L1	tubby	308
☐	L2	L1 and plant	156
☐	L3	L2 and (transgenic or transform?)	119
☐	L4	L3 and stress	43
☐	L5	('20040048249' |'20050120408' |'20030217383' |'20040019925' |'20050108791' |'20030226173' |'20030188330' |'20030121070')!.PN.	8

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10/763,042

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=> s tubby
L1 234 TUBBY

=> s l1 and plant
L2 13 L1 AND PLANT

=> s l1 and (transgenic or transform?)
L3 27 L1 AND (TRANSGENIC OR TRANSFORM?)

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 24 DUP REM L3 (3 DUPLICATES REMOVED)

=> d 1-24 ab

L4 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB Genes showing altered patterns of expression in the brain that are associated with the neurol. changes found in Alzheimer's disease and that can be used in the early diagnosis of the disease, including the incipient form of the disease, are identified. The methods and kits of the invention utilize a set of genes and their encoded proteins that are shown to be correlated with incipient Alzheimer's disease.

L4 ANSWER 2 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB This invention relates to production of cyclic quinone derivs. for use in regulation of gene expression, as relates to prevention or therapy of human diseases. Cyclic quinone synthesis schemes and structures are presented. With the goal of transcription regulation in diseased tissues, gene expression profile data is provided. The intended disease target for this invention is adenocarcinoma of the colon, however the invention claims application in numerous human diseases. Applications of the invention include production of cyclic quinone-based active ingredients in therapeutic agents.

L4 ANSWER 3 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB Mitogen-activated protein (MAP) kinases (e.g., ERK1/2) phosphorylate a variety of target proteins including, for example, several immediate-early gene products (e.g., Fos, Myc, and Jun family proteins). Certain phosphorylation reactions require binding of the MAP kinase to the DEF

domain of the target protein. Inhibitors that block this interaction may be useful therapeutics for human disease, including as antineoplastic agents. This invention provides several advantages over known therapies that directly target the MAP kinase signaling cascade. Typically, most compds. that inhibit the MAP kinase pathway are non-specific and inhibit more than one enzyme, and the targeted inhibited kinases are not available to perform normal physiol. functions necessary for cell survival, whereas therapeutic methods of the present invention inhibit the activation of particular target proteins and leave the MAP kinases enzymically active and available to phosphorylate other non-DEF domain-containing proteins. Thus, DEF domains are identified in a large number of proteins, and the principles of the invention are exemplified using the immediate-early gene, c-Fos. Screening assays useful for identifying compds. that inhibit the MAP kinase-DEF domain interaction are also disclosed.

L4 ANSWER 4 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention provides a large number of cDNA sequences encoding proteins containing transcription factor motifs from Eucalyptus grandis and Pinus radiata. Microarray oligonucleotide probes for the polynucleotides are also provided. The nucleic acids may be used to **transform** plants to regulate gene expression involved in lignin quality and structure, wood composition, plant fiber composition, plant cell division, and plant development.

L4 ANSWER 5 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB The present invention is directed to seed from a **transgenic** plant, wherein the genome of said seed comprises an exogenous polynucleotide comprising a functional portion of an encoding region for a polypeptide provided herein, and wherein plants grown from said seed exhibit an enhanced phenotype as compared to the phenotype of a control plant. Of particular interest are plants wherein the enhanced phenotype is increased yield. A Gateway Destination plant expression vector, pMON65154, was constructed for use in preparation of constructs comprising recombinant polynucleotides for corn **transformation**. Generally, pMON65154 comprises a selectable marker expression cassette comprising a cauliflower mosaic virus 35S promoter operably linked to a gene encoding neomycin phosphotransferase II. The 3' region of the selectable marker expression cassette comprises the 3' region of the Agrobacterium tumefaciens nopaline synthase gene followed 3' by the 3' region of the potato proteinase inhibitor II gene. Similar vectors for use in Agrobacterium-mediated soybean **transformation** systems are constructed where the 35S promoter is replaced with other desirable promoters including a napin promoter and an Arabidopsis SSU promoter. The invention provides 339 nucleic acid sequences and their encoded proteins, such as S-adenosylmethionine decarboxylase or deoxyhyposine synthase, that are expected to yield improved phenotypes. An addnl. 23,471 homologs are identified by BLAST searching of known protein sequences using a proprietary sequence database and the NCIB non-redundant amino acid database.

L4 ANSWER 6 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention relates to the identification and use of gene expression profiles, or patterns, suitable for identification of breast cancer patient populations with different survival outcomes. The gene expression profiles may be embodied in nucleic acid expression, protein expression, or other expression formats, and may be used in the study and/or determination of the prognosis of a patient, including breast cancer survival.

L4 ANSWER 7 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention provides protein and cDNA sequences of 11 novel Arabidopsis **tubby**-like proteins. Disclosed is an isolated nucleic acid that, under stringent conditions, hybridizes to a probe containing one of SEQ ID

NOs:1-11; or its complementary sequence. Also disclosed are (1) a **transformed** cell or a **transgenic** plant containing such a nucleic acid and (2) a **transformed** cell or a **transgenic** plant lacking one or more of SEQ ID NOs:1-11. Also within the scope of the invention are methods for making the **transformed** cells or **transgenic** plants.

L4 ANSWER 8 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB The curcuminoids- and anthocyanins-responsive gene expression profiles in adipocytes have been revealed. The curcuminoids- and anthocyanins-responsive genes are designed to be used as the index markers in the screenings of the substances that can affect the gene expression patterns in obesity and diabetes. These substances can be the candidates of anti-obesity and anti-diabetes drugs. Therefore, the groups of curcuminoids- and anthocyanins-responsive genes are intended to be used as markers in a form of kit such as DNA chip for the screening of anti-obesity and anti-diabetes drugs.

L4 ANSWER 9 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB Housekeeping genes commonly expressed in 35 different human tissues, oligonucleotide probes and DNA microarrays containing them, are disclosed.

L4 ANSWER 10 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 1
AB In mammals, **TUBBY**-like proteins play an important role in maintenance and function of neuronal cells during postdifferentiation and development. We have identified a **TUBBY**-like protein gene family with 11 members in Arabidopsis, named AtTLP1-11. Although seven of the AtTLP genes are located on chromosome I, no local tandem repeats or gene clusters are identified. Except for AtTLP4, reverse transcription-PCR analysis indicates that all these genes are expressed in various organs in 6-week-old Arabidopsis. AtTLP1, 2, 3, 6, 7, 9, 10, and 11 are expressed ubiquitously in all the organs tested, but the expression of AtTLP5 and 8 shows dramatic organ specificity. These 11 family members share 30% to 80% amino acid similarities across their conserved C-terminal **tubby** domains. Unlike the highly diverse N-terminal region of animal **TUBBY**-like proteins, all AtTLP members except AtTLP8 contain a conserved F-box domain (51-57 residues). The interaction between AtTLP9 and ASK1 (Arabidopsis Skp1-like 1) is confirmed via yeast (Saccharomyces cerevisiae) two-hybrid assays. Abscisic acid (ABA)-insensitive phenotypes are observed for two independent AtTLP9 mutant lines, whereas **transgenic** plants overexpressing AtTLP9 are hypersensitive to ABA. These results suggest that AtTLP9 may participate in the ABA signaling pathway.

L4 ANSWER 11 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB This invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which are correlated with (and thus able to discriminate between) cells in various stages and/or grades of breast cancer. Broadly defined, these stages are non-malignant vs. malignant, but may also be viewed as normal vs. atypical (optionally including reactive and pre-neoplastic) vs. cancerous. Another definition of the stages is normal vs. precancerous (e.g. atypical ductal hyperplasia or atypical lobular hyperplasia) vs. cancerous (e.g., carcinoma in situ such as ductal carcinoma in situ (DCIS) and/or lobular carcinoma in situ (LCIS)) vs. invasive (e.g. carcinomas such as invasive ductal carcinoma and/or invasive lobular carcinoma). The signature profiles are identified based upon multiple sampling of reference breast tissue samples from independent cases of breast cancer and provide a reliable set of mol. criteria for identification of cells as being in one or more particular stages and/or grades of breast cancer. The gene CRIP1 is especially prominent and thus may be a potential biomarker for the detection of breast cancer

including the pre-malignant stage of atypical ductal hyperplasia. The epithelium-specific transcription factor ELF5 is also noteworthy since it maps to chromosome 11p13-15, a region subject to frequent loss of heterzygosity and rearrangement in multiple carcinoma including breast cancer.

L4 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB A drug discovery method is provided for selecting a compound selected from the group consisting of a small organic substance, a biopharmaceutical, or an antibody or part thereof. The method comprises the steps of (i) expressing one or more receptors on a cell membrane, such as, e.g., an exterior cell surface of a cell, (ii) contacting one or more expressed receptors with a test compound or a selection of test compds. (libraries), and (iii) selecting one or more compds. based on its ability to bind one or more receptors. The step of expressing the one or more receptors comprises capturing one or more receptors on the exterior cell surface in a conformation that predominantly enables binding or interaction with a ligand, and the conformation that predominantly enables binding or interaction with a ligand is provided by modification of one or more receptors by a method comprising at least one of the following: (a) fusion with any protein which keeps the receptor in the desired conformation such as, e.g. an arrestin, a modified arrestin, a G-protein or a modified G-protein, (b) site-directed mutagenesis, and (c) deletion. The receptors may be captured on the exterior cell surface by at least one of the following: (d) interaction of the receptor with a scaffolding protein, optionally, with a scaffolding protein network and (e) means for blocking receptor internalization, e.g. by co-expression of a mutated dynamin or a modified arrestin or by use of chems. such as, e.g., sucrose and/or Tris. Thus, by coexpressing of either the wild-type receptor or by modifying the receptor by engineering for example a recognition motif for a strong binder into its structure (for example, a PDZ recognition motif at its C-terminal end), and coexpression of this with a scaffolding protein such as PSD-95 or a modified scaffolding protein which interacts with the cytoskeleton at the cell surface or is made to be closely associated with the membrane through a lipid anchor, a high level of surface expression can be ensured, which will benefit its use in the drug discovery process. As a result of the strong tendency of the scaffolding proteins to interact with each other, just the cotransfection with one or more appropriate scaffolding proteins or modified scaffolding protein may also lead to the formation of patches with high local concns of the receptor or modified receptor, which will be highly beneficial in the drug discovery process where they are used initially to select binding mols. The method is exemplified by expression of the NK1 receptor in an agonist high-affinity binding form at the surface of transfected cells through fusion with arrestin or the N-terminal fragment of arrestin.

L4 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB Disclosed herein are 92 cDNA sequences that encode novel human polypeptides that are members of various protein families. Also disclosed are polypeptides encoded by these nucleic acid sequences, and antibodies, which immunospecifically-bind to the polypeptide, as well as derivs., variants, mutants, or fragments of the aforementioned polypeptide, polynucleotide, or antibody. The invention further discloses therapeutic, diagnostic, and research methods for diagnosis, treatment, and prevention of disorders involving any one of these novel human nucleic acids and proteins.

L4 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB This invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which are correlated with (and thus able to discriminate between) cells in various stages and/or grades of breast cancer. Broadly defined, these stages are non-malignant vs. malignant, but may also be viewed as normal vs. atypical (optionally including reactive and pre-neoplastic) vs. cancerous. Another definition

of the stages is normal vs. precancerous (e.g. atypical ductal hyperplasia or atypical lobular hyperplasia) vs. cancerous (e.g., carcinoma in situ such as ductal carcinoma in situ (DCIS) and/or lobular carcinoma in situ (LCIS)) vs. invasive (e.g. carcinomas such as invasive ductal carcinoma and/or invasive lobular carcinoma). The signature profiles are identified based upon multiple sampling of reference breast tissue samples from independent cases of breast cancer and provide a reliable set of mol. criteria for identification of cells as being in one or more particular stages and/or grades of breast cancer. The gene CRIP1 is especially prominent and thus may be a potential biomarker for the detection of breast cancer including the pre-malignant stage of atypical ductal hyperplasia. The epithelium-specific transcription factor ELF5 is also noteworthy since it maps to chromosome 11p13-15, a region subject to frequent loss of heterzygosity and rearrangement in multiple carcinoma including breast cancer.

L4 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention claims nucleic acid and polypeptide sequences for a new alternative splice variant of human gene TUB (**TUBBY**), which lacks exon 12 of wild-type human TUB but includes new exons 13 and 14 at its 3'-end. This alternative splice variant encodes a variant TUB protein that is structurally different from the wild-type TUB protein at the C-terminus. The invention also claims a mol. containing the antigen-binding portion of an antibody specific for the variant TUB polypeptide and methods of using the mol. to detect the variant TUB polypeptide. Further, the invention claims recombinant nucleic acids encoding the TUB protein isoform and **transformed** host cells. In addition, the invention claims oligonucleotide probes and methods for detecting mRNAs of this TUB isoform. The inventors have also discovered a TUB antisense gene (TUB-AS) which overlaps with the TUB variant in two regions (TUB exon 4 with TUB-AS exon 12 and TUB exon 14 with TUB-AS exon 2). MRNAs which hybridized to TUB-AS exons 1-3 cDNA probes were detected in mouse tissues.

L4 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB The present invention pertains to novel inhibitors of cyclin-dependent kinases (CDKs), particularly CDK/cyclin complexes, which inhibitors can be used to control proliferation and/or differentiation of cells in which the inhibitors are introduced. The invention provides six novel fusion proteins of protein p27 and p16.

L4 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AB Our previous studies have characterized Dexamethasone (Dex)-induced apoptotic signaling pathways in multiple myeloma (MM) cells; however, related transcriptional events are not fully defined. In the present study, gene expression profiles of Dex-treated MM cells were determined using oligonucleotide arrays. Dex triggers early transient induction of many genes involved in cell defense/repair-machinery. This is followed by induction of genes known to mediate cell death and repression of growth/survival-related genes. The mol. and genetic alterations associated with Dex resistance in MM cells are also unknown. We compared the gene expression profiles of Dex-sensitive and Dex-resistant MM cells and identified a number of genes which may confer Dex-resistance. Finally, gene profiling of freshly isolated MM patient cells validates our in vitro MM cell line data, confirming an in vivo relevance of these studies. Collectively, these findings provide insights into the basic mechanisms of Dex activity against MM, as well as mechanisms of Dex-resistance in MM cells. These studies may therefore allow improved therapeutic uses of Dex, based upon targeting genes that regulate MM cell growth and survival.

L4 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
AB Once a mutation in the gene tub was identified as the cause of obesity, retinal degeneration and hearing loss in **tubby** mice, it became increasingly evident that the members of the tub gene family (tulps) influence maintenance and function of the neuronal cell lineage.

Suggested mol. functions of **tubby**-like proteins include roles in vesicular trafficking, mediation of insulin signaling and gene transcription. The mechanisms through which tub functions in neurons, however, have yet to be elucidated. Here we report the positional cloning of an auditory quant. trait locus (QTL), the modifier of **tubby** hearing 1 gene (moth1), whose wildtype alleles from strains AKR/J, CAST/Ei and 129P2/OlaHsd protect **tubby** mice from hearing loss. Through a **transgenic** rescue experiment, we verified that sequence polymorphisms in the neuron-specific microtubule-associated protein 1a gene (Mtap1a) observed in the susceptible strain C57BL/6J (B6) are crucial for the hearing-loss phenotype. We also show that these polymorphisms change the binding efficiency of MTAP1A to postsynaptic d. mol. 95 (PSD95), a core component in the cytoarchitecture of synapses. This indicates that at least some of the observed polymorphisms are functionally important and that the hearing loss in C57BL/6J-tub/tub (B6-tub/tub) mice may be caused by impaired protein interactions involving MTAP1A. We therefore propose that tub may be associated with synaptic function in neuronal cells.

L4 ANSWER 19 OF 24 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

AB Purpose: To identify the gene responsible for photoreceptor degneration in the classical recessive mutant mouse, Purkinje cell degeneration (pcd). Methods: Here we report the phenotypic characterization, genetic mapping and identification of mutations in four pcd alleles (pcd1J, pcd2J, pcd3J and pcdsid). Results: The pcd mouse exhibits prominent adult-onset degeneration of cerebellar Purkinje cells, retinal photoreceptors, thalamic and olfactory bulb neurons and has defective spermatogenesis. In retina, the first signs of photoreceptor degeneration in pcd mice include a large number of extracellular vesicles adjacent to inner segments during the third postnatal week. This unique feature of photoreceptor degeneration has been found in five other mutant mouse strains exhibiting transient vesicle accumulation in photoreceptor inner segments: rds, **tubby**, tubp1, P347S rho **transgenic**, and kinesin-II null mice. The progressive degeneration of photoreceptors in pcd mice resembles that seen in late onset retinitis pigmentosa (RP). Conclusion: These studies elucidate novel mechanisms underlying photoreceptor degenerative diseases in humans and mice.

L4 ANSWER 20 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AB The present invention provides a vector system that is useful for the generation of mutations in a recombination-based construction method. The invention further includes the incorporation of mutations generated by the method of the present invention into mouse embryonic stem cells and **transgenic** mice.

L4 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AB A novel mouse protein associated with obesity, cDNA encoding it, its recombinant expression, and antibody against it are disclosed. Also provided are diagnostic, preventive or therapeutic agents for obesity, vision impairment, or hearing disorders containing the protein or DNA, and a method for screening for compds. which modify the effect or expression of the protein. CDNA for the protein was cloned from a mouse embryo cDNA library, and was used to **transform** E. coli cells for recombinant expression.

L4 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AB There is considerable evidence that significant factor underlying the individual variability in response to disease, therapy and prognosis lies in a person's genetic make-up. There have been numerous examples relating that polymorphisms within a given gene can alter the functionality of the protein encoded by that gene thus leading to a variable physiol. response. In order to bring about the integration of genomics into medical practice and enable design and building of a technol. platform which will enable the everyday practice of mol. medicine a way must be invented for the DNA

sequence data to be aligned with the identification of genes central to the induction, development, progression and outcome of disease or physiol. states of interest. According to the invention, the number of genes and their configurations (mutations and polymorphisms) needed to be identified in order to provide critical clin. information concerning individual prognosis is considerably less than the 100,000 thought to comprise the human genome. The identification of the identity of the core group of genes enables the invention of a design for genetic profiling technologies which comprises of the identification of the core group of genes and their sequence variants required to provide a broad base of clin. prognostic information - "genostics". The "Genostic" profiling of patients and persons will radically enhance the ability of clinicians, healthcare professionals and other parties to plan and manage healthcare provision and the targeting of appropriate healthcare resources to those deemed most in need. The use of this invention could also lead to a host of new applications for such profiling technologies, such as identification of persons with particular work or environment related risk, selection of applicants for employment, training or specific opportunities or for the enhancing of the planning and organization of health services, education services and social services.

L4 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AB There is considerable evidence that significant factor underlying the individual variability in response to disease, therapy and prognosis lies in a person's genetic make-up. There have been numerous examples relating that polymorphisms within a given gene can alter the functionality of the protein encoded by that gene thus leading to a variable physiol. response. In order to bring about the integration of genomics into medical practice and enable design and building of a technol. platform which will enable the everyday practice of mol. medicine a way must be invented for the DNA sequence data to be aligned with the identification of genes central to the induction, development, progression and outcome of disease or physiol. states of interest. According to the invention, the number of genes and their configurations (mutations and polymorphisms) needed to be identified in order to provide critical clin. information concerning individual prognosis is considerably less than the 100,000 thought to comprise the human genome. The identification of the identity of the core group of genes enables the invention of a design for genetic profiling technologies.

L4 ANSWER 24 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AB The present invention pertains to novel inhibitors of cyclin-dependent kinases (CDKs), particularly CDK/cyclin complexes, which inhibitors can be used to control proliferation and/or differentiation of cells in which the inhibitors are introduced. Transfection systems are described expressing a fusion protein containing an inhibitor polypeptide comprising cyclin-dependent kinase (CDK)-binding motifs from more than one protein and, optionally, an endothelialization polypeptide such as the HIV-1 tat protein. Fusion proteins and their encoding nucleic acid sequences are provided for p27 and p16, INK4 proteins containing CDK-binding motifs, and for tat fragments fused to p27 and/or p16. These fusion proteins successfully inhibit Cdk2/cyclin E, Cdk4/Cyclin D1, and Cdc2/cyclinB with IC50 values in the nanomolar range.